RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/857,581B
Source: IFW16
Date Processed by STIC: 3/1/05

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 03/01/2005
PATENT APPLICATION: **US/09/857,581B** TIME: 15:18:42

Input Set : **A:\BB1339 RCE Seq Lst.txt**
Output Set: **N:\CRF4\03012005\I857581B.raw**

<110> APPLICANT: Fader, Gary M.
Jung, Woosuk
Brian, McGonigle
Odell, Joan T.
Yu, Xiaodan

<120> TITLE OF INVENTION: Nucleic Acid Fragments Encoding Isoflavone Synthase

<130> FILE REFERENCE: BB1339RCE

C--> **<140> CURRENT APPLICATION NUMBER: US/09/857,581B**

C--> **<141> CURRENT FILING DATE: 2001-06-05**

(pg. 6)

<150> PRIOR APPLICATION NUMBER: PCT/US00/01,772
<151> PRIOR FILING DATE: 2000-01-26
<150> PRIOR APPLICATION NUMBER: 60/117,769
<151> PRIOR FILING DATE: 1999-01-27
<150> PRIOR APPLICATION NUMBER: 60/144,783
<151> PRIOR FILING DATE: 1990-07-20
<150> PRIOR APPLICATION NUMBER: 60/156,094
<151> PRIOR FILING DATE: 1999-09-24

<160> NUMBER OF SEQ ID NOS: 66

<170> SOFTWARE: PatentIn version 3.3

<210> SEQ ID NO: 1
<211> LENGTH: 1756
<212> TYPE: DNA
<213> ORGANISM: Glycine max

<400> SEQUENCE: 1

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cgtcccacac caagtgcaaa atcaaaagca cttcgccacc tcccaaaccc tccaagccca 180
aagcctcgtc ttcccttcat tggccacctt cacctcttaa aagataaact tctccactat 240
gcactcatcg atctctccaa aaagcatggc cccttattct ctctctcctt cggctccatg 300
ccaaccgtcg ttgcctccac ccctgagttg ttcaagctct tcctccaaac ccacgaggca 360
acttccttca acacaaggtt ccaaacctct gccataagac gcctcactta cgacaactct 420
gtggccatgg ttccattcgg accttactgg aagttcgtga ggaagctcat catgaacgac 480
cttctcaacg ccaccaccgt caacaagctc aggcctttga ggacccaaca gatccgcaag 540
ttccttaggg ttatggccca aagcgcagag gcccagaagc cccttgacgt caccgaggag 600
cttctcaaat ggaccaacag caccatctcc atgatgatgc tcggcgaggc tgaggagatc 660
agagacatcg ctcgcgaggt tcttaagatc ttcggcgaat acagcctcac tgacttcatc 720
tggcctttga agtatctcaa ggttggaaag tatgagaaga ggattgatga catcttgaac 780
aagttcgacc ctgtcgttga aagggtcatc aagaagcgcc gtgagatcgt cagaaggaga 840
aagaacggag aagttgttga gggcgaggcc agcggcgtct tcctcgacac tttgcttgaa 900
ttcgctgagg acgagaccat ggagatcaaa attaccaagg agcaaatcaa gggccttgtt 960
gtcgactttt tctctgcagg gacagattcc acagcggtgg caacagagtg ggcattggca 1020
gagctcatca acaatcccag ggtgttgcaa aaggctcgtg aggaggtcta cagtgttgtg 1080
ggcaaagata gactcgttga cgaagttgac actcaaaacc ttccttacat tagggccatt 1140

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gagtgtgaga ttaatgggta tgtgatccca gagggagcat tggttctttt caatgtttgg   1260
caagtaggaa gggaccccaa atactgggac agaccatcag aattccgtcc cgagaggttc   1320
ttagaaactg gtgctgaagg ggaagcaggg cctcttgatc ttaggggcca gcatttccaa   1380
ctcctcccat ttgggtctgg gaggagaatg tgccctggtg tcaatttggc tacttcagga   1440
atggcaacac ttcttgcatc tcttatccaa tgctttgacc tgcaagtgct gggccctcaa   1500
ggacaaatat tgaaaggtga tgatgccaaa gttagcatgg aagagagagc tggcctcaca   1560
gttccaaggg cacatagtct cgtttgtgtt ccacttgcaa ggatcggcgt tgcatctaaa   1620
ctccttttctt aattaagata atcatcatat acaatagtag tgtcttgcca tcgcagttgc   1680
tttttatgta ttcataatca tcatttcaat aaggtgtgac tggtacttaa tcaagtaatt   1740
aaggttacat acatgc                                                   1756
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<211> LENGTH: 521
<212> TYPE: PRT
<213> ORGANISM: Glycine max
<400> SEQUENCE: 2
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1               5                  10                  15
His Leu Arg Pro Thr Pro Ser Ala Lys Ser Lys Ala Leu Arg His Leu
            20                  25                  30
Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
        35                  40                  45
His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
    50                  55                  60
Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met Pro Thr
65                  70                  75                  80
Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
                85                  90                  95
Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
            100                 105                 110
Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
        115                 120                 125
Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
    130                 135                 140
Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
145                 150                 155                 160
Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp Val Thr
                165                 170                 175
Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
            180                 185                 190
Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
        195                 200                 205
Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Tyr Leu
    210                 215                 220
Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
225                 230                 235                 240
Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
                245                 250                 255
Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly Val Phe
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Input Set : **A:\BB1339 RCE Seq Lst.txt**
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124             260                 265                 270
126 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
127         275                 280                 285
129 Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
130     290                 295                 300
132 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
133 305                 310                 315                 320
135 Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val Tyr Ser
136                 325                 330                 335
138 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
139             340                 345                 350
141 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
142         355                 360                 365
144 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
145     370                 375                 380
147 Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp Gln Val
148 385                 390                 395                 400
150 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
151                 405                 410                 415
153 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
154             420                 425                 430
156 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
157         435                 440                 445
159 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
160     450                 455                 460
162 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
163 465                 470                 475                 480
165 Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
166                 485                 490                 495
168 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
169             500                 505                 510
171 Ile Gly Val Ala Ser Lys Leu Leu Ser
172         515                 520
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 27
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Oligonucleotide primer used in construction of WHT1
182 <400> SEQUENCE: 3
183 cgggatccat gcaaccggaa accgtcg                                          27
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 32
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Oligonucleotide primer used in construction of yeast strain
WHT1
193 <400> SEQUENCE: 4
194 ccggaattct caccaaacat cacggaggta tc                                    32
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RAW SEQUENCE LISTING DATE: 03/01/2005
PATENT APPLICATION: **US/09/857,581B** TIME: 15:18:42

Input Set : **A:\BB1339 RCE Seq Lst.txt**
Output Set: **N:\CRF4\03012005\I857581B.raw**

196 <210> SEQ ID NO: 5
197 <211> LENGTH: 47
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Oligonucleotide primer
204 <400> SEQUENCE: 5
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207 <210> SEQ ID NO: 6
208 <211> LENGTH: 35
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Oligonucleotide primer
215 <400> SEQUENCE: 6
216 ggccagtgaa ttgtaatacg actcactata gggcg 35
218 <210> SEQ ID NO: 7
219 <211> LENGTH: 24
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Oligonucleotide primer
226 <400> SEQUENCE: 7
227 aaaattagcc tcacaaaagc aaag 24
229 <210> SEQ ID NO: 8
230 <211> LENGTH: 27
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Oligonucleotide primer
237 <400> SEQUENCE: 8
238 atataaggat tgatagttta tagtagg 27
240 <210> SEQ ID NO: 9
241 <211> LENGTH: 1824
242 <212> TYPE: DNA
243 <213> ORGANISM: Glycine max
245 <400> SEQUENCE: 9
246 ggaaaattag cctcacaaaa gcaaagatca aacaaaccaa ggacgagaac acgatgttgc 60
247 ttgaacttgc acttggttta ttggttttgg ctctgtttct gcacttgcgt cccacaccca 120
248 ctgcaaaatc aaaagcactt cgccatctcc caaacccacc aagcccaaag cctcgtcttc 180
249 ccttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc 240
250 tctccaaaaa acatggtccc ttattctctc tctactttgg ctccatgcca accgttgttg 300
251 cctccacacc agaattgttc aagctcttcc tccaaacgca cgaggcaact tccttcaaca 360
252 caaggttcca aacctcagcc ataagacgcc tcacctatga tagctcagtg gccatggttc 420
253 ccttcggacc ttactggaag ttcgtgagga agctcatcat gaacgacctt cccaacgcca 480
254 ccactgtaaa caagttgagg cctttgagga cccaacagac ccgcaagttc cttagggtta 540
255 tggcccaagg cgcagaggca cagaagcccc ttgacttgac cgaggagctt ctgaaatgga 600
256 ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc 660
257 gcgaggttct taagatcttt ggcgaataca gcctcactga cttcatctgg ccattgaagc 720

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Input Set : **A:\BB1339 RCE Seq Lst.txt**
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258 atctcaaggt tggaaagtat gagaagagga tcgacgacat cttgaacaag ttcgaccctg    780
259 tcgttgaaag ggtcatcaag aagcgccgtg agatcgtgag gaggagaaag aacggagagg    840
260 ttgttgaggg tgaggtcagc ggggttttcc ttgacacttt gcttgaattc gctgaggatg    900
261 agaccatgga gatcaaaatc accaaggacc acatcgaggg tcttgttgtc gacttttttct   960
262 cggcaggaac agactccaca gcggtggcaa cagagtgggc attggcagaa ctcatcaaca   1020
263 atcctaaggt gttggaaaag gctcgtgagg aggtctacag tgttgtggga aaggacagac   1080
264 ttgtggacga agttgacact caaaaccttc cttacattag agcaatcgtg aaggagacat   1140
265 tccgcatgca cccgccactc ccagtggtca aaagaaagtg cacagaagag tgtgagatta   1200
266 atggatatgt gatcccagag ggagcattga ttctcttcaa tgtatggcaa gtaggaagag   1260
267 accccaaata ctgggacaga ccatcggagt tccgtcctga gaggttccta gagacagggg   1320
268 ctgaagggga agcagggcct cttgatctta ggggacaaca ttttcaactt ctcccatttg   1380
269 ggtctgggag gagaatgtgc cctggagtca atctggctac ttcgggaatg gcaacacttc   1440
270 ttgcatctct tattcagtgc ttcgacttgc aagtgctggg tccacaagga cagatattga   1500
271 agggtggtga cgccaaagtt agcatggaag agagagccgg cctcactgtt ccaagggcac   1560
272 atagtcttgt ctgtgttcca cttgcaagga tcggcgttgc atctaaactc ctttcttaat   1620
273 taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa   1680
274 ggtctcgttc atctactttt tatgaagtat ataagccctt ccatgcacat tgtatcatct   1740
275 cccatttgtc ttcgtttgct acctaaggca atctttttttt ttttagaatc acatcatcct   1800
276 actataaact atcaatcctt atat                                         1824
278 <210> SEQ ID NO: 10
279 <211> LENGTH: 521
280 <212> TYPE: PRT
281 <213> ORGANISM: Glycine max
283 <400> SEQUENCE: 10
284 Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
285 1               5                   10                  15
287 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
288             20                  25                  30
290 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
291         35                  40                  45
293 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
294     50                  55                  60
296 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
297 65                  70                  75                  80
299 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
300                 85                  90                  95
302 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
303             100                 105                 110
305 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
306         115                 120                 125
308 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr
309     130                 135                 140
311 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
312 145                 150                 155                 160
314 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
315                 165                 170                 175
317 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
318             180                 185                 190
320 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/01/2005
PATENT APPLICATION: **US/09/857,581B** TIME: 15:18:43

Input Set : **A:\BB1339 RCE Seq Lst.txt**
Output Set: **N:\CRF4\03012005\I857581B.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:66; Xaa Pos. 10,16,23,25,39,48,60,73,74,95,96,102,110,112,117,118,121
Seq#:66; Xaa Pos. 122,124,129,140,147,159,162,166,170,175,183,187,191,209
Seq#:66; Xaa Pos. 219,223,253,259,263,264,268,272,285,292,293,295,301,306
Seq#:66; Xaa Pos. 311,312,325,328,329,334,342,377,381,385,387,393,394,402
Seq#:66; Xaa Pos. 404,413,422,428,429,435,447,453,459,485

VERIFICATION SUMMARY DATE: 03/01/2005
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0
M:341 Repeated in SeqNo=66